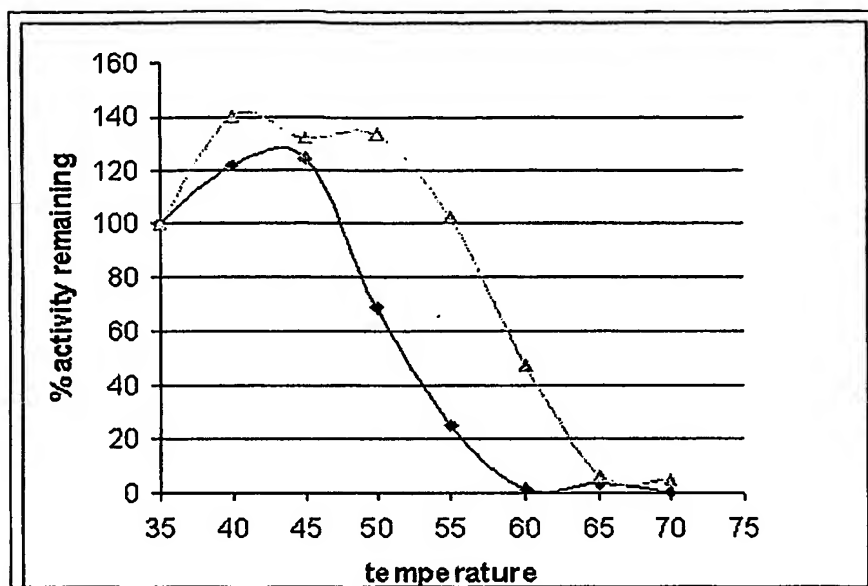
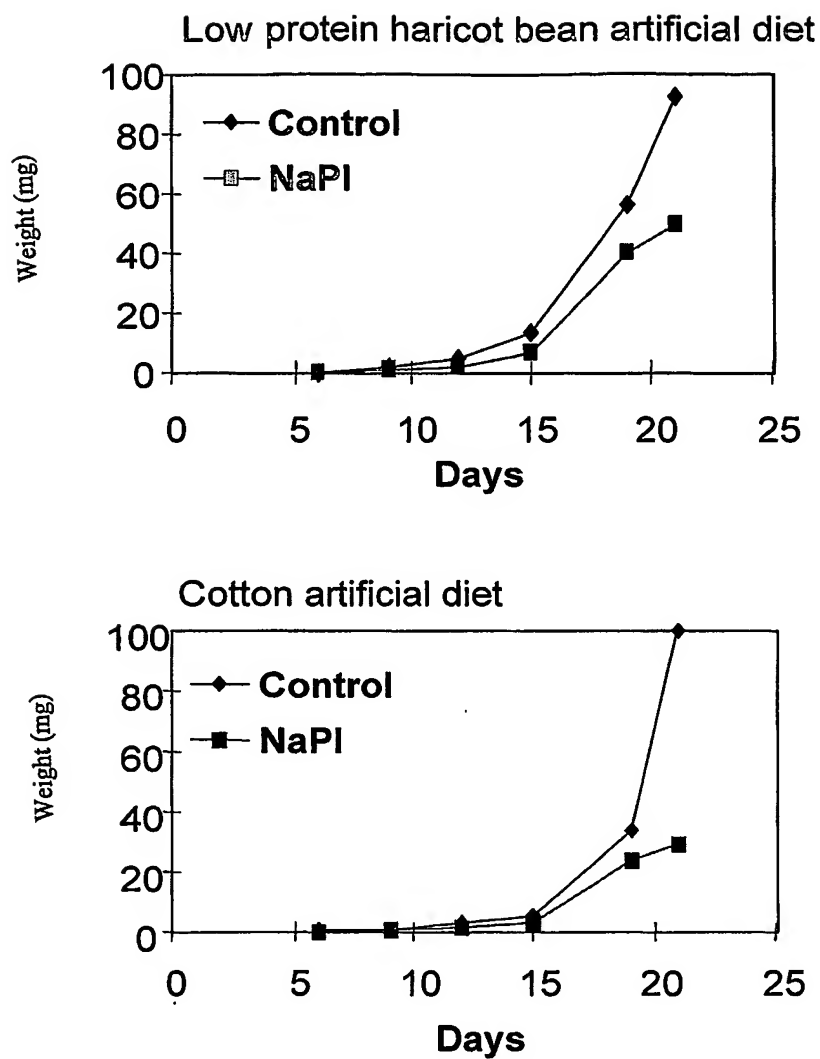


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**Figure 1**

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**Figure 2A**

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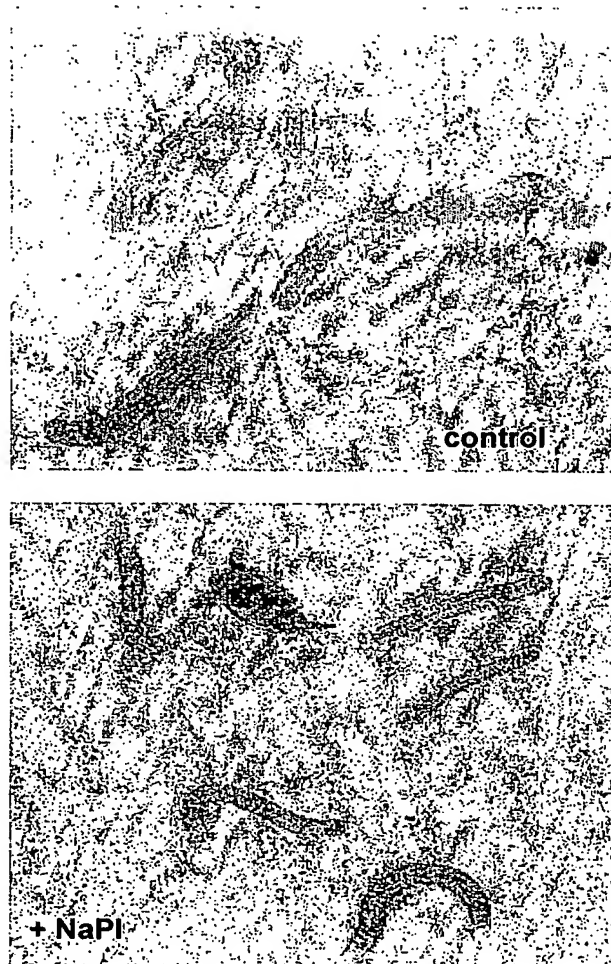
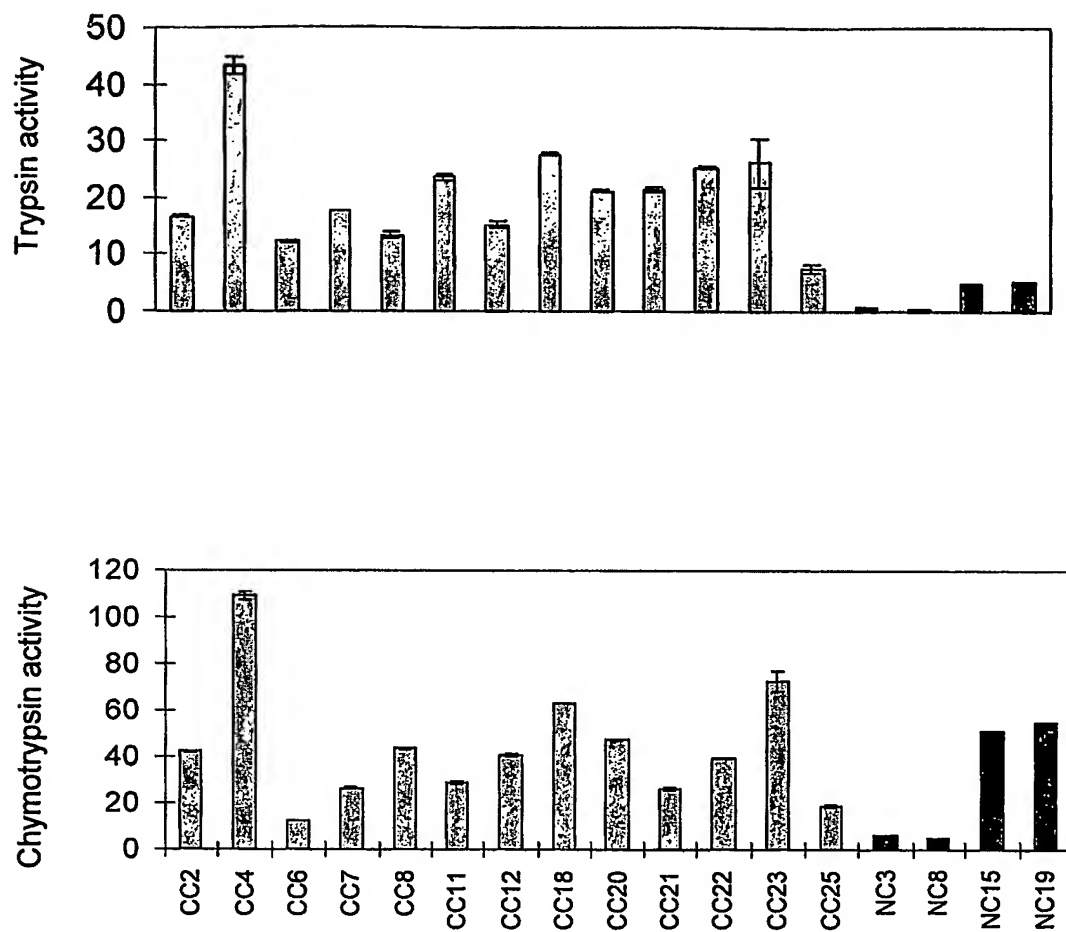


Figure 2B

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**Figure 2C**

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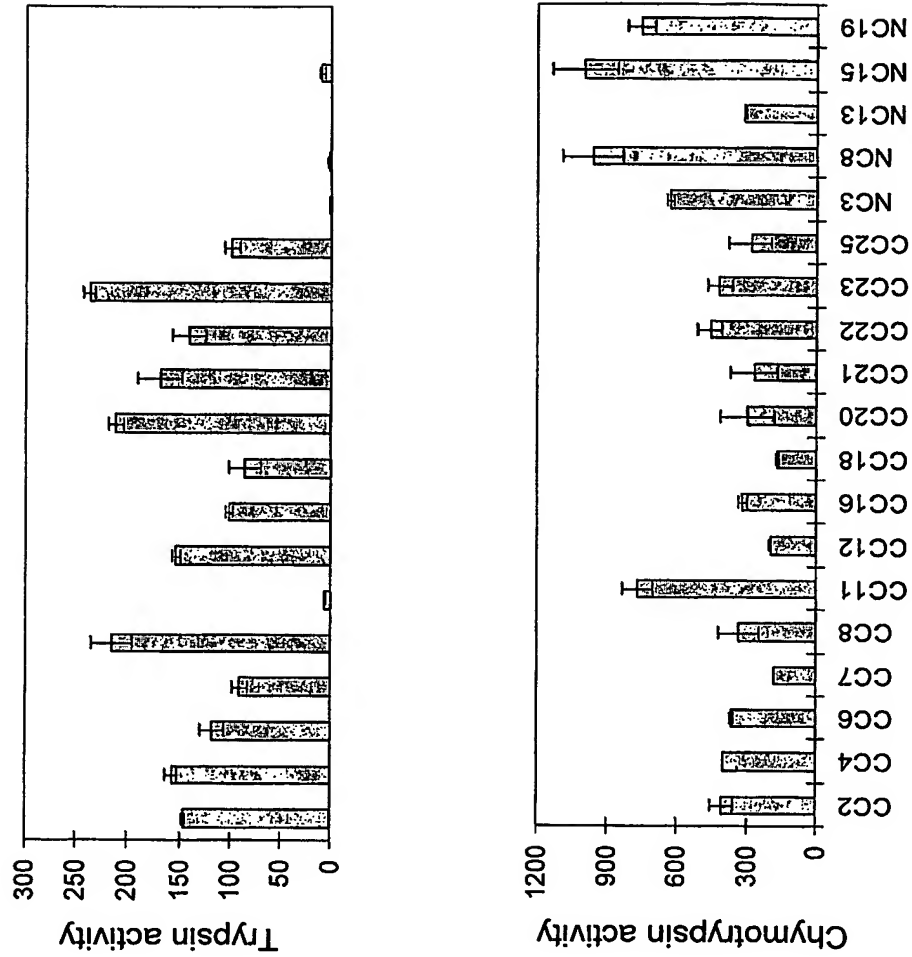
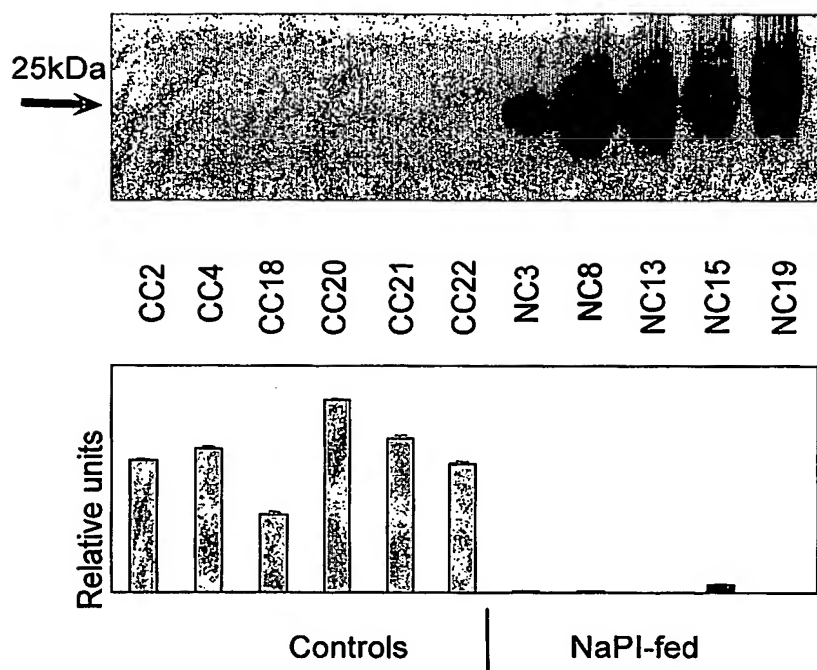
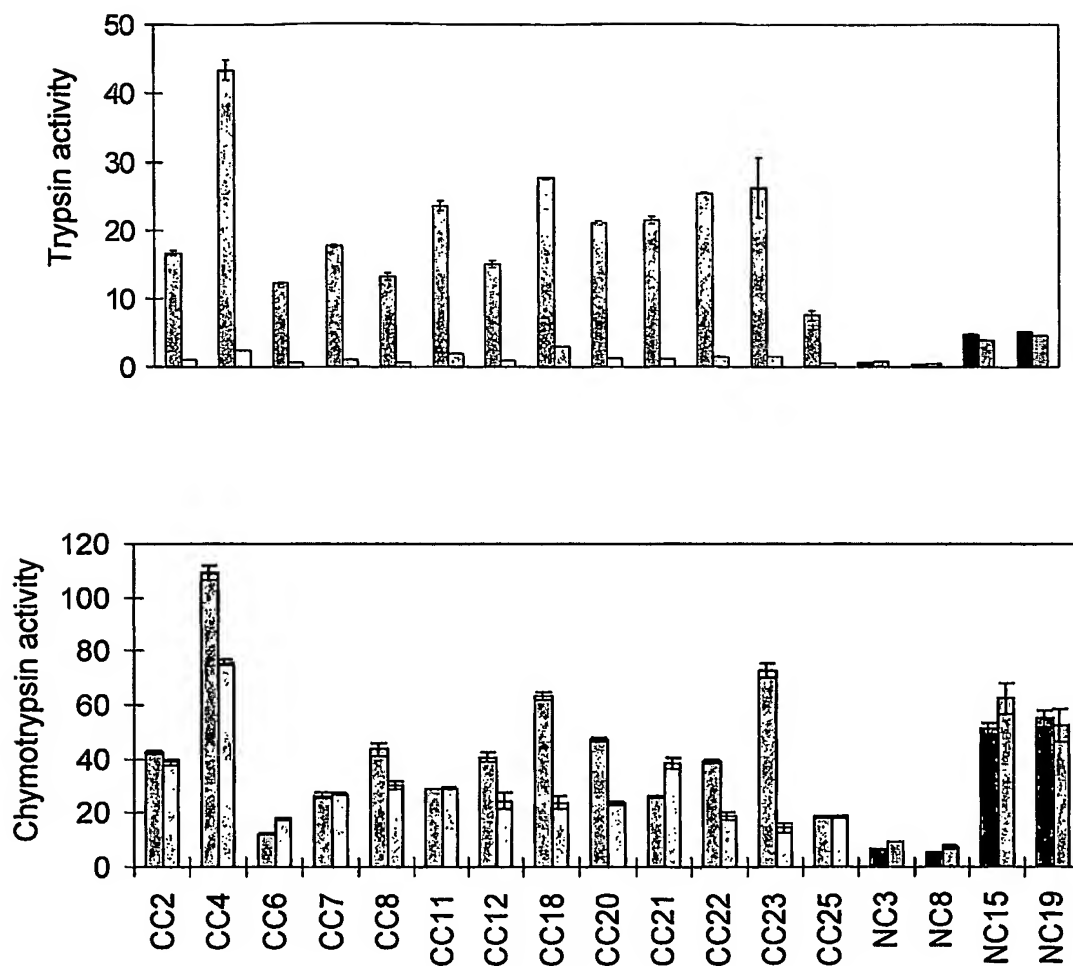


Figure 2D

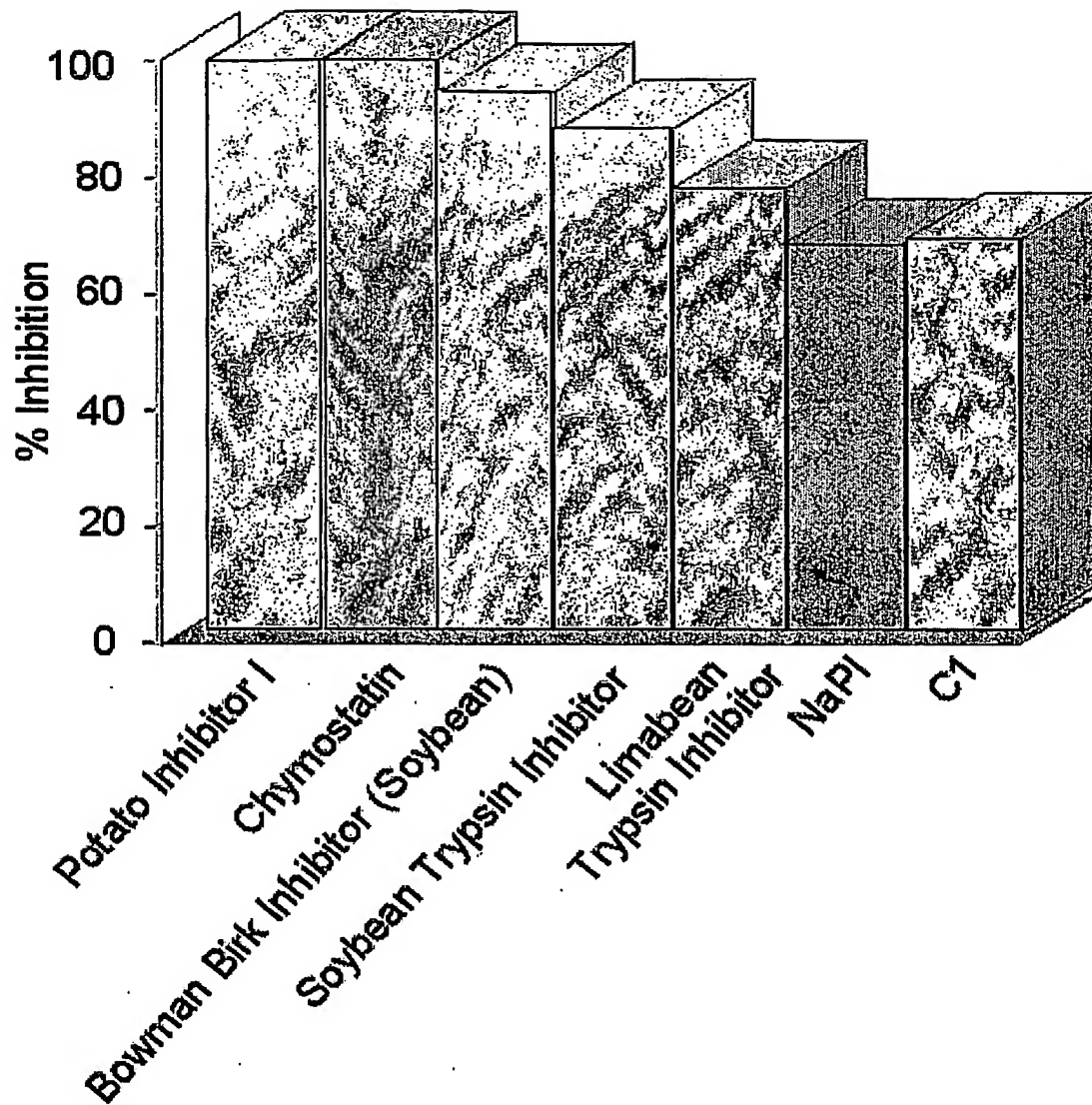
6/36

**Figure 2E**

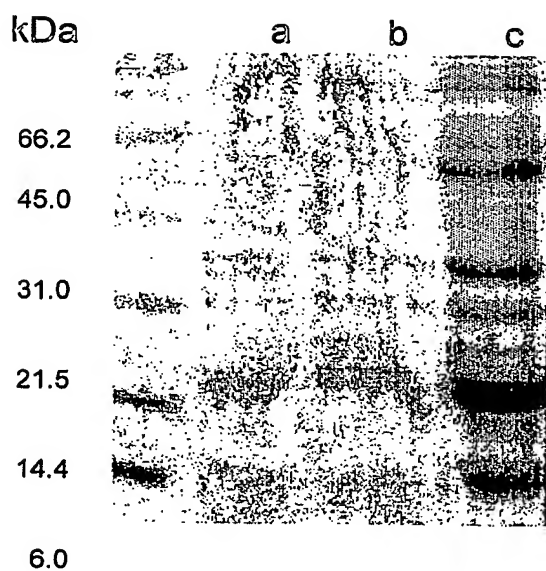
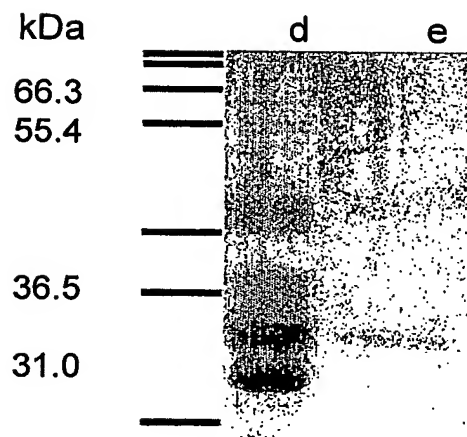
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**Figure 2F**

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**Figure 3**

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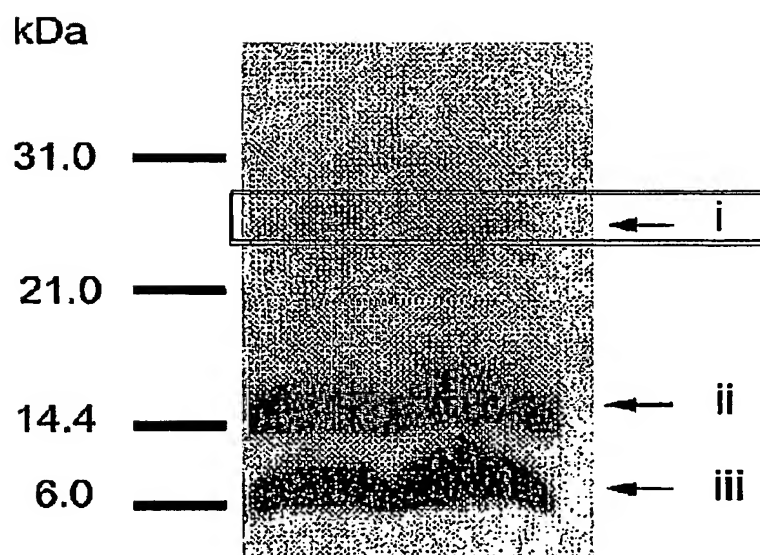
**Figure 4A****Figure 4B**

21.5
*Hp*CHY1 IVGGSTSSLGATPYQ

Figure 4C

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A

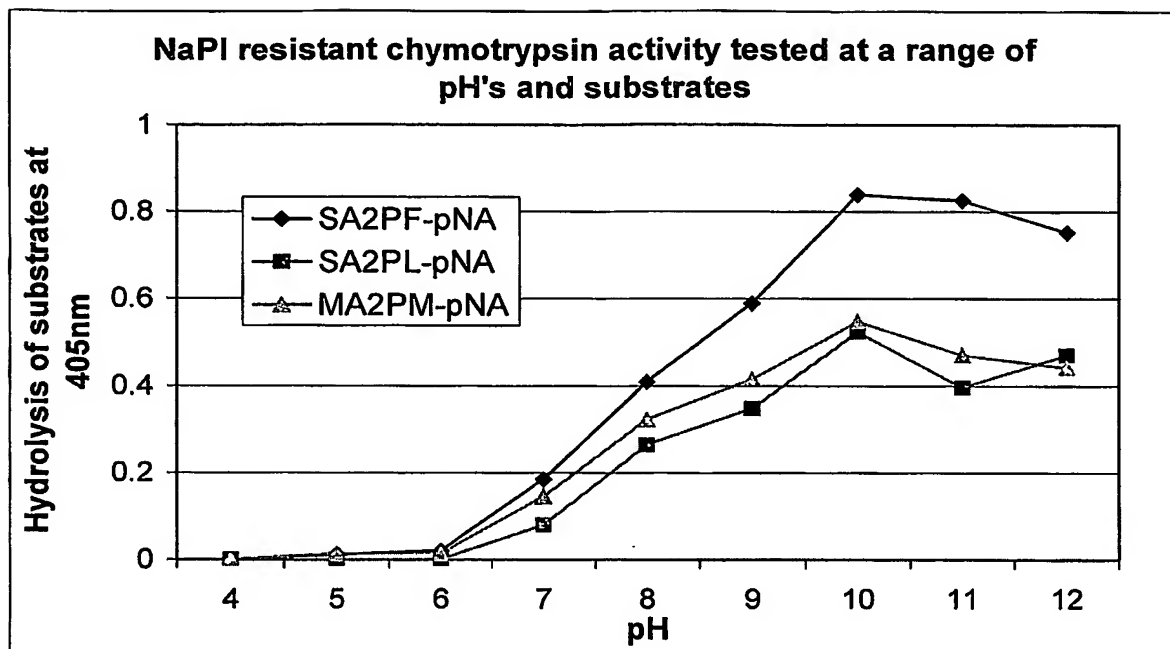


B

i	<i>Rech1a</i>	IVGGSLSVGQIPYQAGLVIDLAGGQAVCGGSLISA
	<i>Rech1b</i>	IVGGSISSIGQIPYGAGLVIDFAGGQAVC
	<i>Rech1c</i>	IVGGSTSSVGQFPYQAGLLASFAGGQAVC
	<i>Rech1d</i>	IVGGSVTTLDAYPTIAGLVYNFAGGQAVC

Figure 5

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**Figure 6**

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CAA72966 MKLLAVTLLAFAAVVSARNIDLEDVIDLEDITAYDYHTKIGIPLAEKIRA
 CAA72959 ---LAVTLLAFAAVVSARNIDLEDVIDLEDITAYDYHTKIGIPLAEKIRA
 CAA72960 MKLLAVTLLAFAAIVSARNIDLEDVIDLEDITAYDYHTKIGIPLAEKIRA
 CAA72958 -----INHEAVVDLEDITAYGYHTKVGIPLAEEIIRI
 CAA72952 MKLFLGVCLTLAVAVSAVEIATPD----ADSPVFGYHAKFGIAEAARIKS
 CAA72951 -----

FWY79→ FWG1→

CAA72966 AEEEAERNPSRIVGGSTSSLGAFPYQAGLLATFASGQGVCGGSLLNNRRV
 CAA72959 AEEEAERNPSRIVGGSTSSLGAFPYQAGLLATFASGQGVCGGSLLNNRRV
 CAA72960 AEEEAERNPSRIVGGSSISLGAFPYQAGLLATFASGQGVCGGSLLNNRRV
 CAA72958 AELEASRNPSRIVGGSSASLGFPYQAGLLLINLPLGQSVCGGSLLNQRRV
 CAA72952 AEEVQSFNGQRIVGGSSITNIANVPYQAGLVITIFIFQSVCGASLISHNRL
 CAA72951 -----HNKWW

CAA72966 LTAAHCWFDGRNQARSFTVVLGSRVLFSGGTRLNTASVVMHGSWNPNIIR
 CAA72959 LTAAHCWFDGRNQARSFTVVLGSRVLFSGGTRLNTASVVMHGSWNPNIIR
 CAA72960 LTAAHCWFDGRNQARSFTVVLGSRVLFSGGTRLNTASVVMHGSWNPNIIR
 CAA72958 LTAAHCWFDGRNQANSLTVILGSINLYFGGTRLNSNSVVMHGSWNPNIIR
 CAA72952 VTAAHCKSDGVL TANSFTVVLGSNTLFFGGTRINTNDVVMHPNWNPTAA
 CAA72951 LTAAHCLANRITFVVRFLTNLTRPEILVESANKYIHPDYDEIRAG-VQT

CAA72966 NDIAMINLPSNVATSGNIAP--IALPSGNELNNNFNGATAVASGFGGLARD
 CAA72959 NDIAMINLPSNVATSGNIAP--IALPSGNELNNNFNGATAVASGFGGLARD
 CAA72960 NDIAMINLPSNVATSGNIAP--IALPSGNELNNNFNGATAVASGFGGLARD
 CAA72958 NDIAMINLPSNVGTSNNIAP--IALPSGNELNNQFAGFTATASGFGTRTD
 CAA72952 NDIAVLRIS--VSFSNVIQP--IALPSGDELNNLFVGANALASGFGRTSD
 CAA72951 ADLALVGLDHHIEYSANVQPSRLMSSAQKNINYE--GIQMIVSGFGRTDD

FWY72→

CAA72966 GGSVDGN---LRHVNLPVITNAVCTVSFP-GIIQSS-NICTSG--ANGRS
 CAA72959 GGSVDGN---LRHVNLPVITNAVCTVSFP-GIIQSS-NICTSG--ANGRG
 CAA72960 GGSVDGN---LRHVNLPVITNAVCTVSFP-GIIQSS-NICTSG--ANGRS
 CAA72958 GGSVSPT---LNHVNLPVITNNVCWQSFP-LYIQSS-NICTSG--ANGRS
 CAA72952 SGSIGTN-QQLSSVTIPVITNAQCAAVYGSGFVHAS-NICTSG--AGGKG
 CAA72951 LWNGGAASEILLWVYQRGVSNEECLRWYPTSQVIKEETICAGYWDNPSQS

←RVG4

CAA72966 TCQGDSGGPLVVTSN-NRRILIGVTSFGSARGCQVGSPAAAFARVTSFISW
 CAA72959 TCQGDSGGPLVVTSN-NRRILIGVTPFGSARGCQVGSPAAAFARVTSFISW
 CAA72960 TCQGDSGGPLVVTSN-NRRILIGVTSFGSARGCQVGSPAAAFARVTSFISW
 CAA72958 TCQGDSGGPLVVTSN-NRRILIGVTSFGSDRGVCQVGAPAAAFARVTSYISW
 CAA72952 TCNGDSGGPLAVDSN-NRKILIGVTSYGAQAGCAAGFPAAAFARVTSFVDW
 CAA72951 SCQGDSGGPLTIIDADGERTQVGIVSFGSTAGCNSPFPSGYVRPGHYHDW

←RVY72

CAA72966 INQRL-----
 CAA72959 INQRL-----
 CAA72960 INNLL-----
 CAA72958 INQRL-----
 CAA72952 VQSQ-----
 CAA72951 FTEVTGINFDWSDAIIPGSSESSSSSESSEPSSESSESSEEDGANPSSS

CAA72966 -----
 CAA72959 -----
 CAA72960 -----
 CAA72958 -----
 CAA72952 -----
 CAA72951 EEDGSNPSSEEDAGSPPSEEEEEAPEKVRVVEY

Figure 7

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Primer Name	Sequence 5'-3'
FWG1	TCC CTT ACC AGG C (GCT) GTC [SEQ ID NO:38]
RVG4	TCT GGC GAA GGC AGC AGG [SEQ ID NO:39]
Y79Fw	CTG CTA GCC TCG GAC AAT TC [SEQ ID NO:40]
Y72Fw	CTG GAG TGC AGA CTG CTG AC [SEQ ID NO:41]
Y72Rv	GGA TGA TGG CGT CGC TGT CC [SEQ ID NO:42]

Figure 8

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HpF1Apcr	PYQAGL	VITIFIFQSVCGASLIPHNRLVTAAHCKSDGVLTAANSFTVVLGS	50
HpF1Bpcr	PYQAGL	VITIFIFQSVCGASLISHNRLVTAAHCKFDGVMTANSFTVVLGS	50
HpF2Apcr	PYQAGL	LANFASGQGVCGSLLNQRRVLTAAHCWFDGRNQARSFTVVLGS	50
HpF3pcr	ASLGQF	PYQAGLLINLPLGQSVCGSLLNQRRVLTAAHCWFDGRNQATSLTVILGS	57
HpF4pcr		-----	
HpF1Apcr		NTLFFGGTRINTNDVVMHPNWNPSTAANDIAVMRISS-VSFSNVIQPIAL	99
HpF1Bpcr		NTLFFGGTRINTNDVVMHPNWNPSTVANDIAVIRISS-IVFNNVIQPIAL	99
HpF2Apcr		VRLFSGGTRLDTASVVMHGSWNPNIIRNDIAMINLPSNVATSGNIAPIAL	100
HpF3pcr		INLFFGGTRLNSNSVVMHGSWNPNIIRNDIAIINLPSNVGTSGNIAPIAL	100
HpF4pcr		-----SGVQTADLALVGLDQEIEYSANVQPSRL	28
HpF1Apcr		PSGDELNNLFVGANALASGFGRTSDGGSIGSNQQ-VSSVTIPVITNDECA	148
HpF1Bpcr		PSGDELNNLFVGANALASGFGRTSDGGIGTNQQ-LSSVTIPVITNAECA	148
HpF2Apcr		PSGNELNNNFNGATATASGFGLARDGGSVDGN---LRHVNLPVITNAVCT	147
HpF3pcr		PSGNELNNQFAGFTATASGFGLTRDGGNVSP---LNHVNLPVITNNVCW	147
HpF4pcr		MSSAQKNINYEGIQMIVSGFGRTDDLWNGGAASEILLWVYQGVSNEECL	78
HpF1Apcr		AVYGS-AFVHSSNICTSGAGG--KGTCNGDSGGPLAIDSNN-EKILIGVT	194
HpF1Bpcr		AVYGP-AFVHDTNICTSGAGG--KGTCNGDSGGPLAVDSND-KKILIGVT	194
HpF2Apcr		VSFP--GIIQSSNICTSGANG--RSTCQGDSGGP-----	177
HpF3pcr		QSFP--LYIQSTNICTSGANG--RGTCQGDSGGPLVVTSSNN-RRILIGVT	192
HpF4pcr		RWYPTSQVIKEQTICAGYWDNPSQSSCQGDSGGPLTIIDADGERTQVGIV	128
HpF1Apcr		SYGAQAGCAAGLPAAAFARK-----	213
HpF1Bpcr		SYGAADGCAAGFPAASPER-----	213
HpF2Apcr		-----	
HpF3pcr		SFGSDRGCVGAPAAAFAR-----	210
HpF4pcr		SFGSTAGCNSPFPSGYVRPGHYHDWFTEVTGINFDWDSDAIT	120

Figure 9

Figure 10A

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HpCh1AI	-----	-----	-----	-----	279
HpCh1BI	-----	-----	-----	-----	292
HpCh2A	-----	-----	-----	-----	295
HpCh2B	-----	-----	-----	-----	295
HpCh3A	-----	-----	-----	-----	234
HpCh4I	-----	-----	-----	-----	297
HpCh4II	CQPPRFPTRT	VPTHLPRRTL	AAPPSEEEEA	PEKVRVVEY	365

Figure 10B

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		F1	F2
[SEQ ID NO:55]	<i>Rech1a</i>	IVGGSLSSVG	QIEFYQAGLVI
[SEQ ID NO:56]	<i>Rech1b</i>	IVGGSTSSVG	QFPYQAGLLA
[SEQ ID NO:57]	<i>Family1a</i>	IVGGSITDIA	NVPYQAGLVI
[SEQ ID NO:58]	<i>Family1b</i>	IVGGSITNIA	NVPYQAGLVI
[SEQ ID NO:59]	<i>Family2a</i>	IVGGSTSSLG	AFPYQAGLLA
[SEQ ID NO:60]	<i>Family2b</i>	IVGGSTSSLG	AFPYQAGLLA
[SEQ ID NO:61]	<i>Family3</i>	IVGGSSASLG	QFPYQAGLSL
[SEQ ID NO:62]	<i>Family4</i>	IVAGWPAVEG	QIPYQGSLRM

Figure 11A

N-terminal sequence of resistant chymotrypsin (Rech 1a)	
IVGGSLSSVGQIEFYQAGLVITLAGGQAVCGGSLISA [SEQ ID NO:9]	
Primer Name	Oligonucleotide sequence 5'-3'
Fw2ResChy = F1	TC(AGCT) GT(AGCT) GG(AGCT) CA(AG) AT(ACT) CC [SEQ ID NO:10]
FwResChym = F2	GT(AGCT) AT(ACT) GA(CT) CT(AGCT) GC(AGCT) GG(AGCT) GG [SEQ ID NO:11]

Figure 11B

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HpCHF5 GTTCACCTCGAGGATTCTATTGATCTGGAAGATATTACCGCTTGGGGATA 50
 V H L E D S I D L E D I T A W G Y
 -40 -24
HpCHF5 CCTCACCAAATTCGGTATTCCAGAAGCTGAGAAAATCCGCAACGCTGAAG 100
 L T K F G I P E A E K I R N A E
 -8
HpCHF5 AAGCTAGCTCTGCTAGCAGGATCGTCGGTGGTTTCATTGTCCAGTGTCCGA 150
 E A S S A S R A L V G G S L S S V G
 -1 +1 +10
HpCHF5 CAGATCCCTTACCAGGCTGGTCTCGTCATTGACTTAGCAGGTGGCCAGGC 200
Q T P Y E O A G L V I D L A G G L O R A
HpCHF5 TGTCTGCGGAGGCTCCCTGATCAGCGCTTCCCGCGTACTGACCGCTGCTC 250
V C G G S V L S A S R V L T A A
HpCHF5 ACTGCTGGTTCGACGGCCAAACAGGCCTGGAGATTACCGTTGTTCTT 300
 H C W F D G Q N Q A W R F T V V L
 #
HpCHF5 GGTTCACACCTTGTTCCTCTGGCGGTACCAGAATCCCTACATCCAATGT 350
 G S T T L F S G G T R I P T S N V
HpCHF5 TGTTATGCACGGAAGCTGGACTCCTAGCCTTATCCGTAACGATGTTGCCG 400
 V M H G S W T P S L I R N D V A
 #
HpCHF5 TAATCAGATTGGGCACCAACGTAGCAACCTCAAACACCATTGCCATCATC 450
 V I R L G T N V A T S N T I A I I
HpCHF5 GCTCTACCCAGCGGCAGCCAGATCAACGAGAACTTCGCCGGTGAAACCGC 500
 A L P S G S Q I N E N F A G E T A
HpCHF5 CCTCGCCTCCGGCTTCGGTCTCACCAGTGACACCGGCAGCATCTCCAGCA 550
 L A S G F G L T S D T G S I S S
HpCHF5 ACCAGGCTCTGAGCCACGTCAACCTGCCAGTGATACCAACGCTGTGTGC 600
 N Q A L S H V N L P V I T N A V C
HpCHF5 AGAAATTCATTCCCCCTGCTGATCCAGGACTCTAACATTTGCACCAGCGG 650
 R N S F P L L I Q D S N I C T S G
HpCHF5 TGCCAACGGCAGGAGCACTTGCCGCGGTGACTCCGGCGGTCTCTCGTCCG 700
 A N G R S T C R G D S G G P L V
 S #
HpCHF5 TCACCAGGAACAACAGACCACTCTTGATCGGTATCACCTCTTTCCGGATCT 750
 V T R N N R P L L I G I T S F G S
HpCHF5 GCCCGCGGTTGCCAAGTTGGATCTCCCGCTGCCTTCGCCAGAGTCACCTC 800
 A R G C Q V G S P A A F A R V T S
HpCHF5 TTACATCAGCTGGATCAACGGCCAGCTCTAAAATATCGAACATTTTGCCA 850
 Y I S W I N G Q L *
HpCHF5 TATCTACAGAGATATTTTGAAATACGTTAATTTAAATAAATATTTTATTT 900
HpCHF5 ATTCAAAAAAAAAAAAAAAAAA 921

Figure 12

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HpCh1AI	IVGGSIITDIANVPYQAGLVITIFI-FQSVCGASLISHNRIVTAAHCKSDG	49
HpCh1BI	IVGGSIITNIANVPYQAGLVITIFI-FQSVCGASLISHNRIVTAAHCKFDG	49
HpCh2A	IVGGSTSSLGAFPYQAGLEAFAS-GQVCGGSLINQRRVLTAAHCFDG	49
HpCh2B	IVGGSTSSLGAFPYQAGLASFAS-GQVCGGSLINQRRVLTAAHCFDG	49
HpCh3	IVGGSSASLGQFPYQAGSLIYS--GQSVCGGSLINQRRVLTAAHCFDG	48
HpCh4I	IVAGWPAVEGQIPYQGSIRMVSAIGVSSCGCSLTHNKWVLTAAHCLAN-	49
HpCh5	IVGGSLSSVGQIPYQAGLVITDLAG-GQAVCGGSLISASRVLTAAHCFDG	49
TrypsinIV	IVGGYTCEENSIPYQVSLNSGSH-----FCGGSLISEQWVVSAAHCY----	42
HpCh1AI	VLTANSFTVVLGSNTLFFGG-TRINTNDVVMHPNWNPS---TAANDTAVM	95
HpCh1BI	VMTANSFTVVLGSNTLFFGG-TRINTNDVVMHPNWNPS---TVANDTAVI	95
HpCh2A	RNQARSFTVVLGSVRLFSGG-TRIDTASVVMHGSWNPN---LIRNDIAMI	95
HpCh2B	RNQARSFTVVLGSVRLFSGG-TRINTASVVMHGSWNPN---LVRNDIAMI	95
HpCh3	RNQATSITVILGSINLFFGG-TRINSNSVVMHGSWNPN---LIRNDIAMI	94
HpCh4I	---RITFVVRFLTNLTRPE-ILVESTNKYTHPEYDEIRAGVQTADLALV	95
HpCh5	QNQAWRFTVVLGSITLFSGG-TRIPTSNVVMHGSWTPS---LIRNDIAMI	95
TrypsinIV	-KTRIQVRLGEHNKVLKLENEQFTNAAKITRHPKYNRD---TIDNDIMET	88
HpCh1AI	RISS-VSFSNVITQPIALPSGDELNNLFVGANALAFGFGRTSDGGSTGSNQ	144
HpCh1BI	RISS-IVYNNVITQPIALPSGDELNNLFVGANALASGFGRTSDGGSTGTNQ	144
HpCh2A	NLPSNVATSGNIAPIALPSGNELNNNFAGATATASGFGGLARDGGSVQGN-	144
HpCh2B	NLPSNVATSGNIAPIALPSGNELNNQFAGATATASGFGGLARDGGVQGN-	144
HpCh3	NLPSNVGTSGNIAPIALPSGNELNNQFAGFTATASGFGGLTRDGGNVSP-	143
HpCh4I	GLDHETEYSANVQPSRLMSSAQKNINYEIQMTIVSGFGRTDDLWNGGAAS	145
HpCh5	RLGTNVATSNITATIALPSGSQINENFAGETALASGFGGLTSDTGSTSSNQ	145
TrypsinIV	KLSSPAVINARVSTISLPIAP-----PAAGTECLISGWNLTLSFGADYPD-	133
HpCh1AI	Q-VSSVITIPVITNDECAAVYG-SAFVHSSNICT--SGAGCKGTGNGDSGG	190
HpCh1BI	Q-LSSVITIPVITNAECAAVYG-PAFVHDINICT--SGAGCKGTGNGDSGG	190
HpCh2A	--LRHVNIPVITNAVCTVSE--PGIIQSSNICT--SGANGRSTCQGDSSG	188
HpCh2B	--LRHVNIPVITNAVCSQSE--PGLIQASNVCT--SGANGRSTCQGDSSG	188
HpCh3	--LNHVNIPVITNNVCWQSF--PLYIQSSNICT--SGANGRGTGQGDSSG	187
HpCh4AI	EILLWVYQRGVSNEECLRWYPTSQVIKEQTICAGYWDNPSQSSCQGDSSG	195
HpCh5	A-LSHVNIPVITNAVCRNSE--PLLIQDSNICT--SGANGRSTCRGDSSG	190
TrypsinIV	E-LKCEAPVLTQAECKASY--PGKITNSMFCVG-FLEGGKDSQORDSSG	179
HpCh1AI	PLAIDSNN--EKILIGVTSYGAQAGCAAGLPAAAFARVTSFVSWVQSQ---	235
HpCh1BI	PLAVDSND--KKILIGVTSYGAADGCAAGFPAAAFARVTSFVSWVQSQ---	235
HpCh2A	PLVVNSNN--RRILIGVTSFGSARGCQVGSPPAAAFARVTSFISWINQRL--	234
HpCh2B	PLVVNSNN--RRILIGVTSFGSARGCQVGSPPAAAFARVTSFISWINQRL--	234
HpCh3	PLVVTSNN--RRILIGVTSFGSARGCQVGAAPAAAFARVTSYISWINQRL--	233
HpCh4I	PLTIDADGERTQSRYCELRHCWNATAHSPQGYVRPGHYHDWFTEVTGI	245
HpCh5	PLVVITRNN--RPLLIGITSFGSARGCQVGSPPAAAFARVTSYISWINQRL--	236
TrypsinIV	PVMCNG-----QLQGVSWGHGCAWK-N-RPGVYTKVYNYVDWIKDTTAA	222
HpCh1AI	-----	235
HpCh1BI	-----	235
HpCh2A	-----	234
HpCh2B	-----	234
HpCh3	-----	233
HpCh4I	NFDWDSDAIIP	256
HpCh5	-----	236
TrypsinIV	NS-----	224

Figure 13

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[SEQ ID NO:71]	DH04_H02 ARMIGERA	VHLEDSDLE	DITAWGYLTK	FGIPEAEKIR	NAEEASSASR
[SEQ ID NO:72]	RECH1A PUNCTIGERA
	DH04_H02 ARMIGERA	IVGGSLSSLG	QIPYQAGLVI	DLSGGQAVCG	GSLISASRVL
	RECH1A PUNCTIGERAA.....
	DH04_H02 ARMIGERA	TAAHCWFDGQ	NQAWRFTVVL	GSTTLFSGGT	RIATSNVVMH
	RECH1A PUNCTIGERAP.....
	DH04_H02 ARMIGERA	GSWTPSLIRN	DVAVIRLGTN	VGTSNTIAII	ALPSGSQINE
	RECH1A PUNCTIGERA
	DH04_H02 ARMIGERA	NFAGETALAS	GFGLTSDSGS	ISSNQALSHV	NLPVITNAVC
	RECH1A PUNCTIGERAT..
	DH04_H02 ARMIGERA	RSSFPLLIQD	SNICTSGANG	RSTCRGDSGG	PLVVTRNSRP
	RECH1A PUNCTIGERA	.N.....N..
	DH04_H02 ARMIGERA	LLIGITSFGS	ARGCQVGSPA	AFARVTSYIS	WINGQ
	RECH1A PUNCTIGERA

Figure 14

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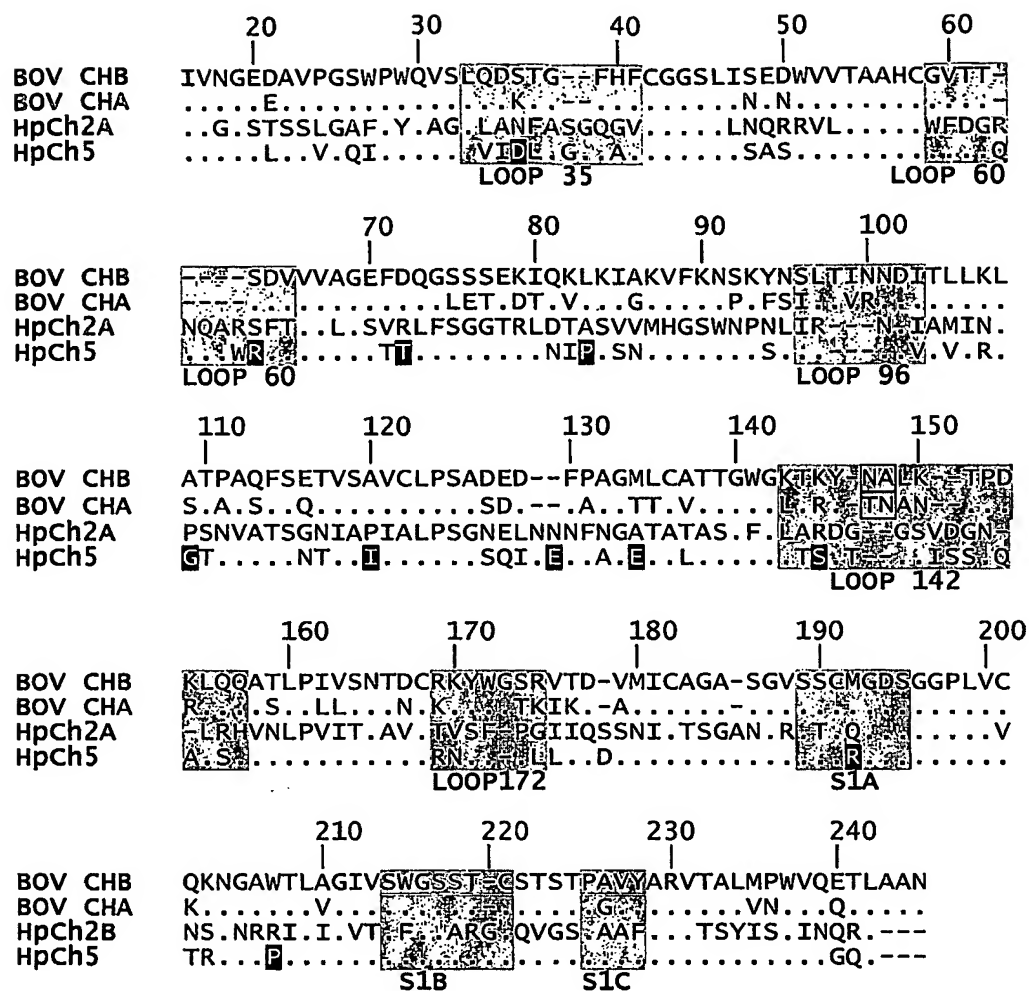


Figure 15

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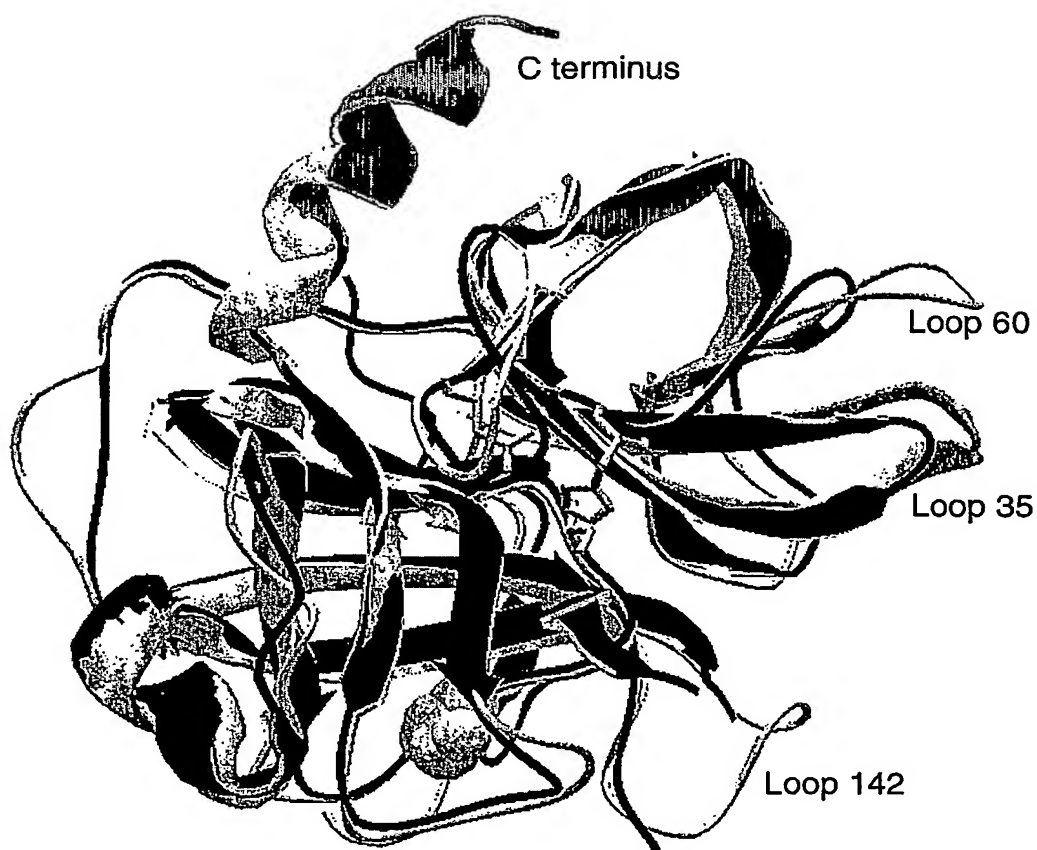


Figure 16

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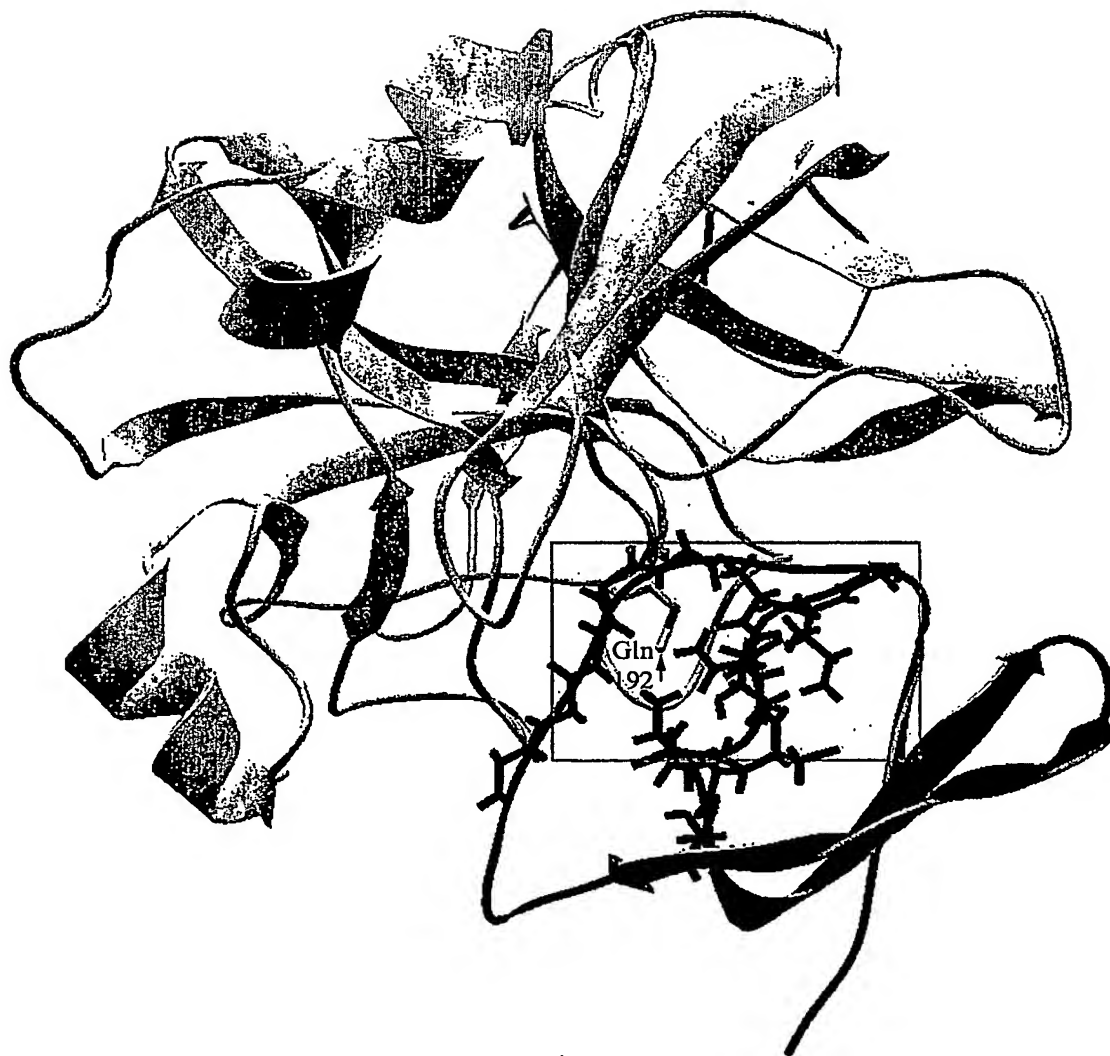


Figure 17

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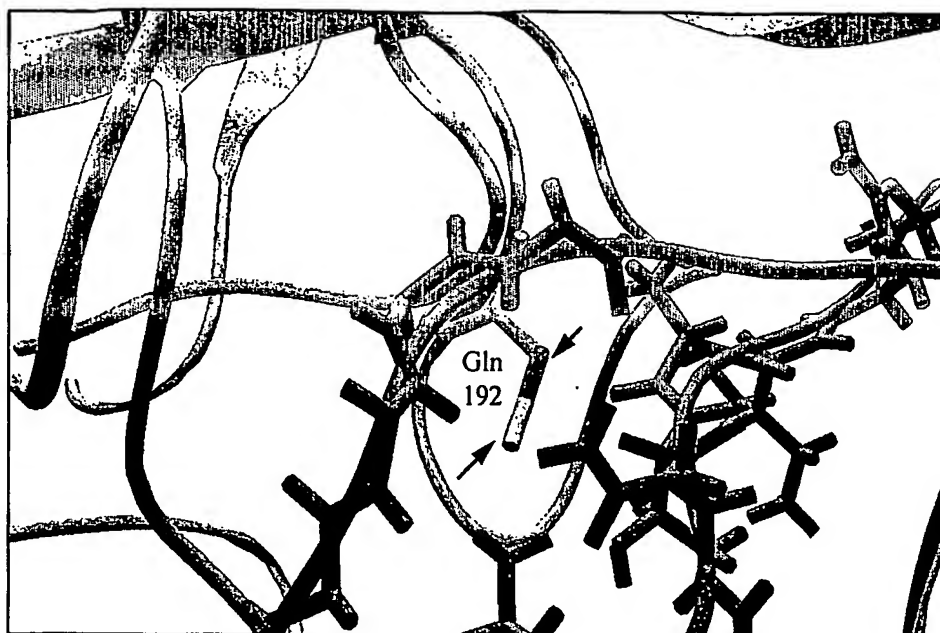


Figure 18A

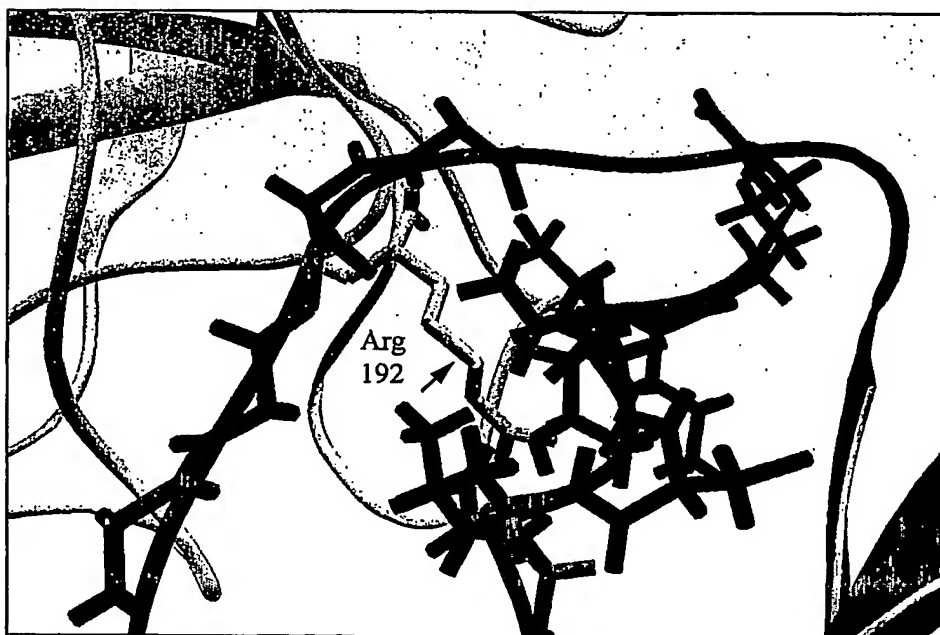


Figure 18B

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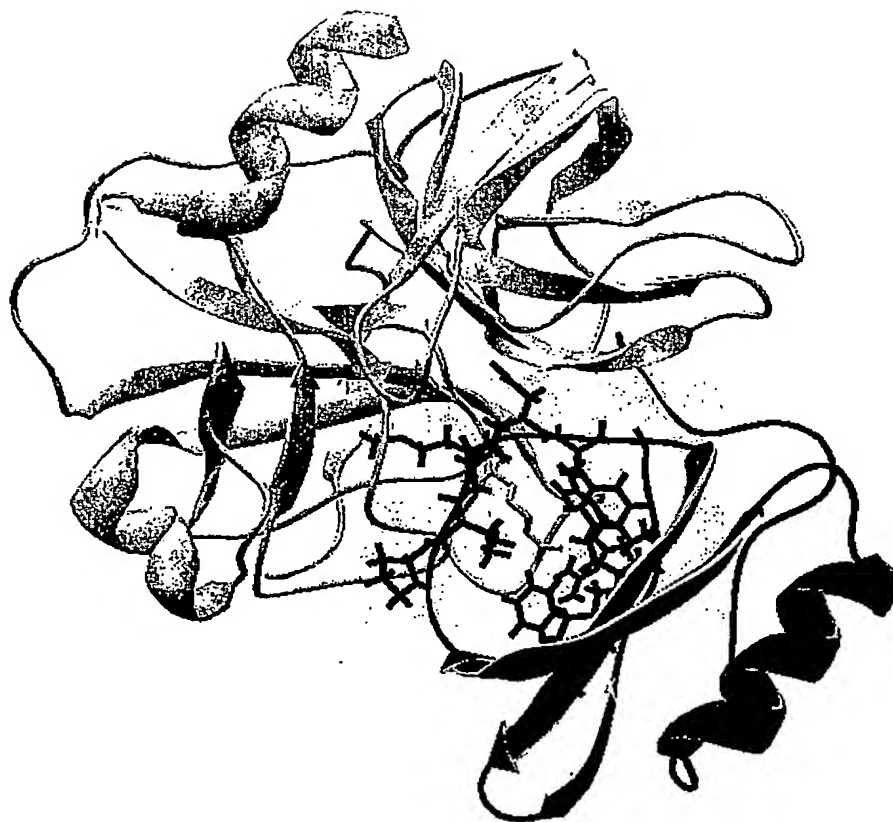


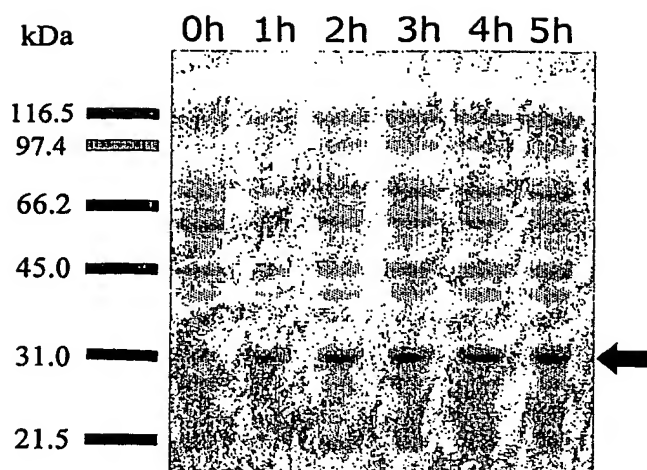
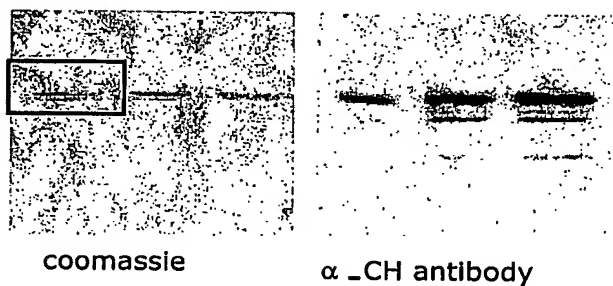
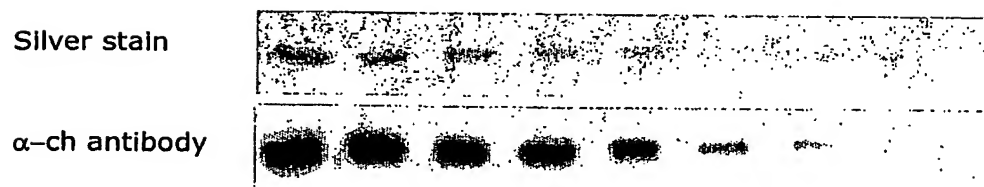
Figure 19A

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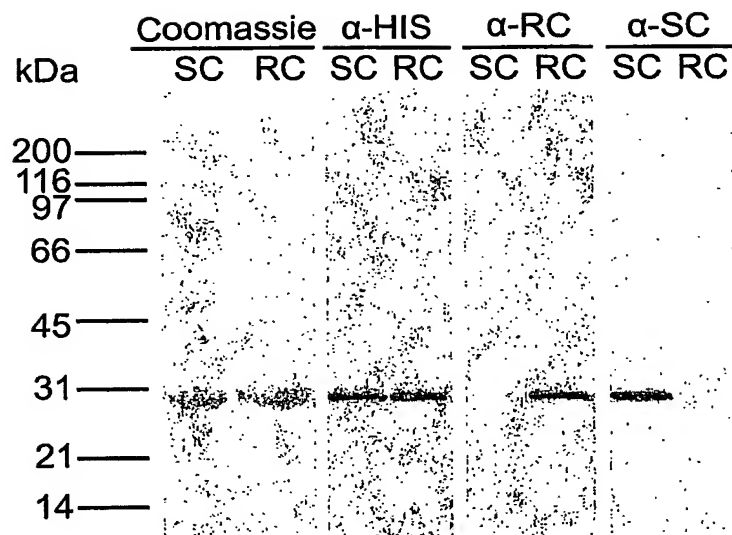


Figure 19B

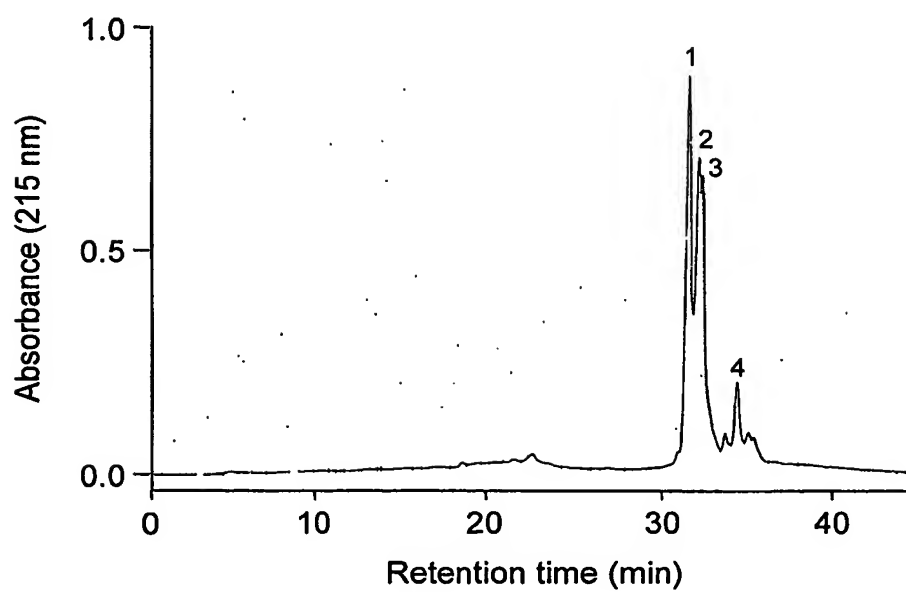
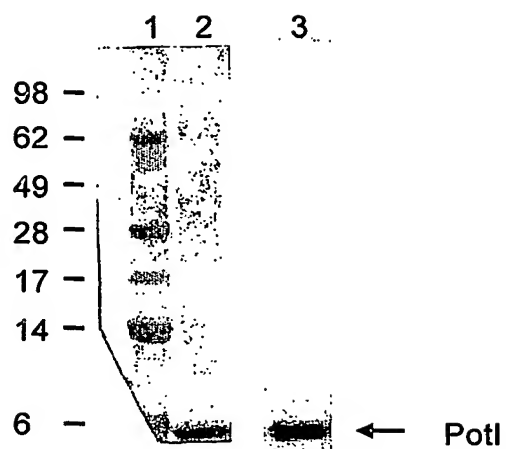
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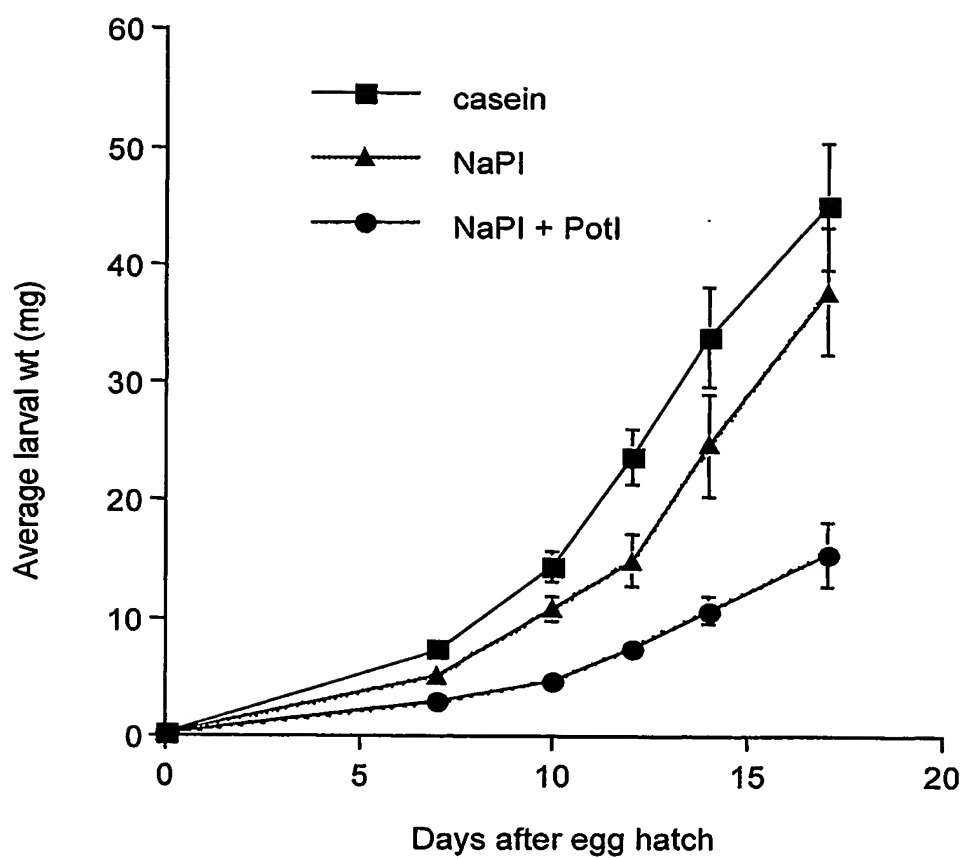
**Figure 20A****Figure 20B****Figure 20C**

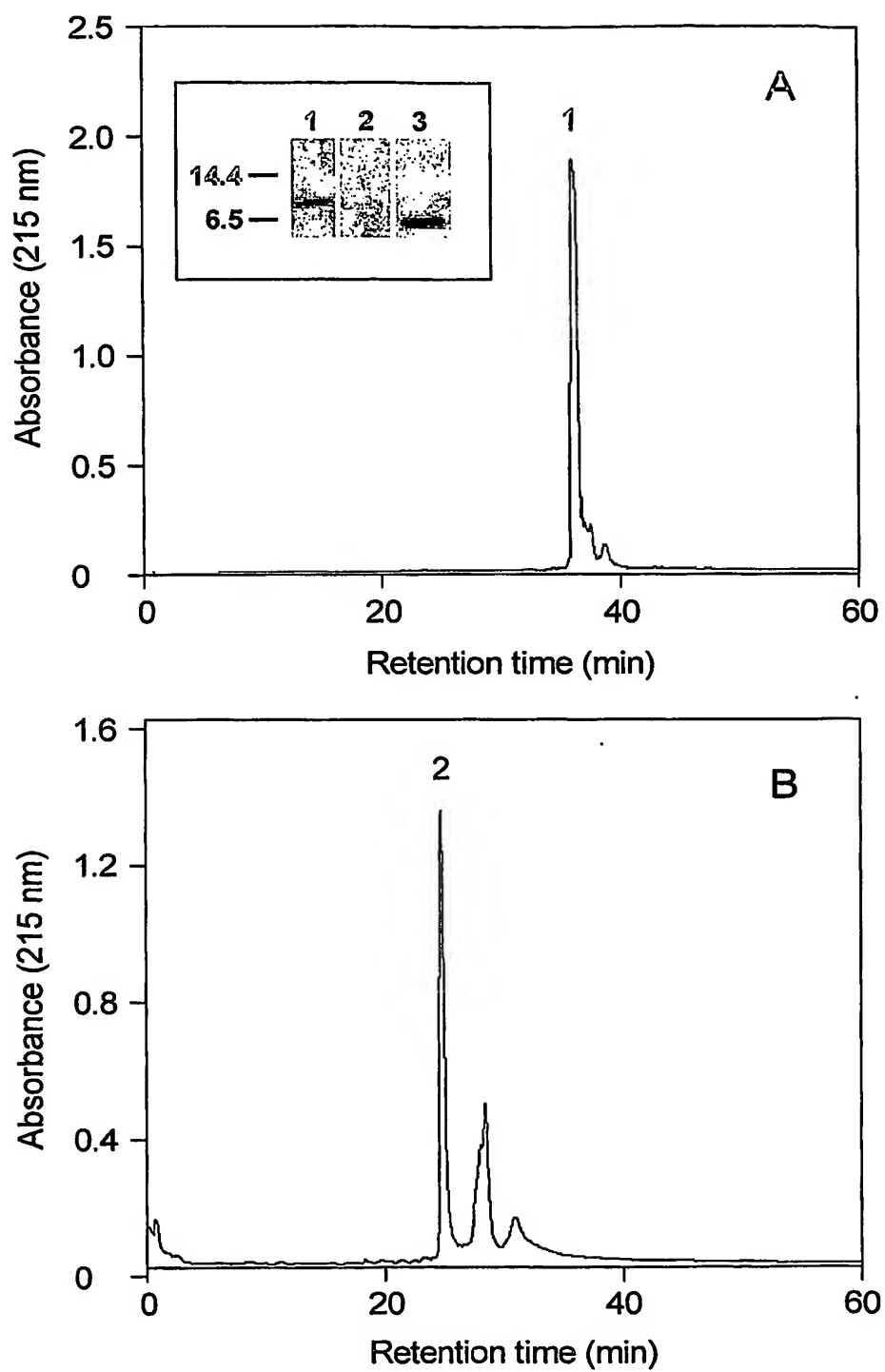
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**Figure 21**

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Figure 22A**Figure 22B**

30/36**Figure 23**

32/36**Figure 25**

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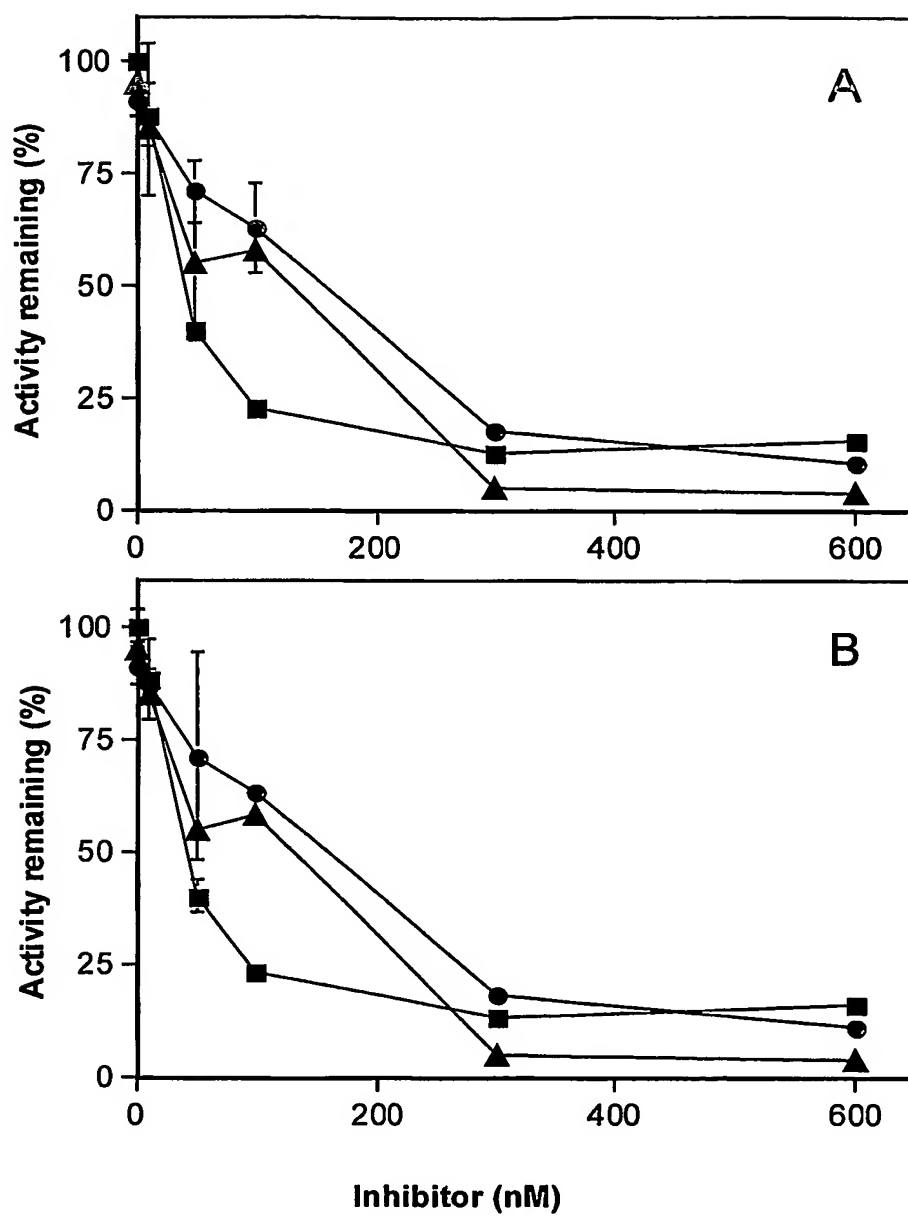
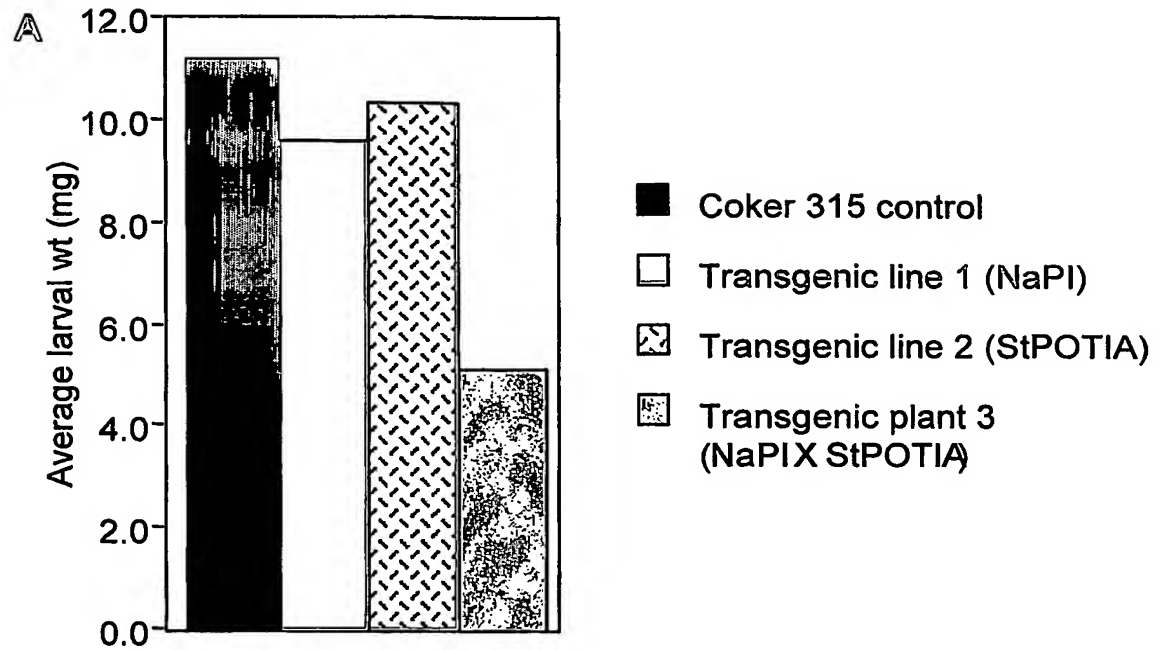
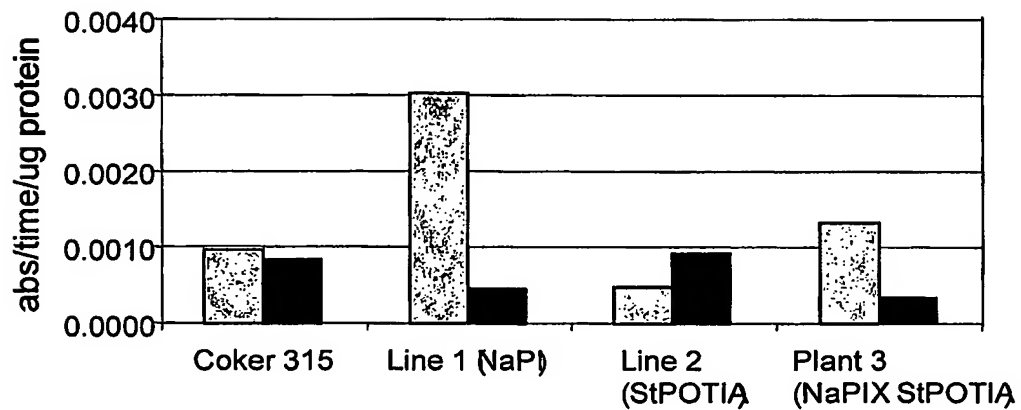


Figure 26

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**Figure 27A****Figure 27B**

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ggatccATGAAACTCTTGGCTGTGACTCTATTGGCTTTCGCCGCGGTTCGTCTCCGCGAGG      60
      M K L L A V T L L A F A A V V S A R

ggatccATGAAACTCTTGGCTGTGACTCTATTGGCtttcg
FwBacRECH2 Primer----->
                        TTGGCTTTCGCCGCGGTTCGTCTCCGCGAGG
                        FwBacRECH2 Primer-----

Aacgg [A] tcccaccatcaccatcaccatGTTACCTCGAGGATTCTATTGATCTGGAAGAT      120
      N G S H H H H H H V H L E D S I D L E D
Aacgg [G] tccc
----->

ATTACCGCTTGGGGATACCTCACCAAATTCGGTATTCCAGAAGCTGAGAAAATCCGCAAC      180
      I T A W G Y L T K F G I P E A E K I R N

GCTGAAGAAGCTAGCTCTGCTAGCAGGATCGTCGGTGGTTCATTGTCCAGTGTCCGACAG      240
      A E E A S S A S R I V G G S L S S V G Q

ATCCCTTACCAGGCTGGTCTCGTCATTGACTTAGCAGGTGGCCAGGCTGTCTGCGGAGGC      300
      I P Y Q A G L V I D L A G G Q A V C G G

TCCCTGATCAGCGCTTCCGCGTACTGACCGCTGCTCACTGCTGGTTCGACGGCCAAAAC      360
      S L I S A S R V L T A A H C W F D G Q N

CAGGCCTGGAGATTACCGTTGTTCTTGGTTCCACCACCTTGTTCTCTGGCGGTACCAGA      420
      Q A W R F T V V L G S T T L F S G G T R

ATCCCTACATCCAATGTTGTTATGCACGGAAGCTGGACTCCTAGCCTTATCCGTAACGAT      480
      I P T S N V V M H G S W T P S L I R N D

GTTGCCGTAATCAGATTGGGCACCAACGTAGCAACCTCAAACACCATTGCCATCATCGCT      540
      V A V I R L G T N V A T S N T I A I I A

CTACCCAGCGGCAGCCAGATCAACGAGAACTTCGCCGGTGAAACCGCCCTCGCCTCCGGC      600
      L P S G S Q I N E N F A G E T A L A S G

TTCGGTCTCACCAGTGACACCGGCAGCATCTCCAGCAACCAGGCTCTGAGCCACGTCAAC      660
      F G L T S D T G S I S S N Q A L S H V N

CTGCCAGTGATCACCAACGCTGTGTGCAGAAATTCATTCCCCCTGCTGATCCAGGACTCT      720
      L P V I T N A V C R N S F P L L I Q D S

AACATTTGCACCAGCGGTGCCAACGGCAGGAGCACTTGCCGCGGTGACTCCGGCGGTCTCT      780
      N I C T S G A N G R S T C R G D S G G P

CTCGTCGTCACCAGGAACAACAGACCACTCTTGATCGGTATCACCTCTTTCGGATCTGCC      840
      L V V T R N N R P L L I G I T S F G S A

CGCGGTGCCAAGTTGGATCTCCCGCTGCCTTCGCCAGAGTCACCTCTTACATCAGCTG      900
      R G C Q V G S P A A F A R V T S Y I S W

GATCAACGGCCAGCTCTAAaagctt      925
      I N G Q L * K L

GATCAACGGCCAGCTCTAAaagctt
<-----RvRECH Primer

```

Figure 28

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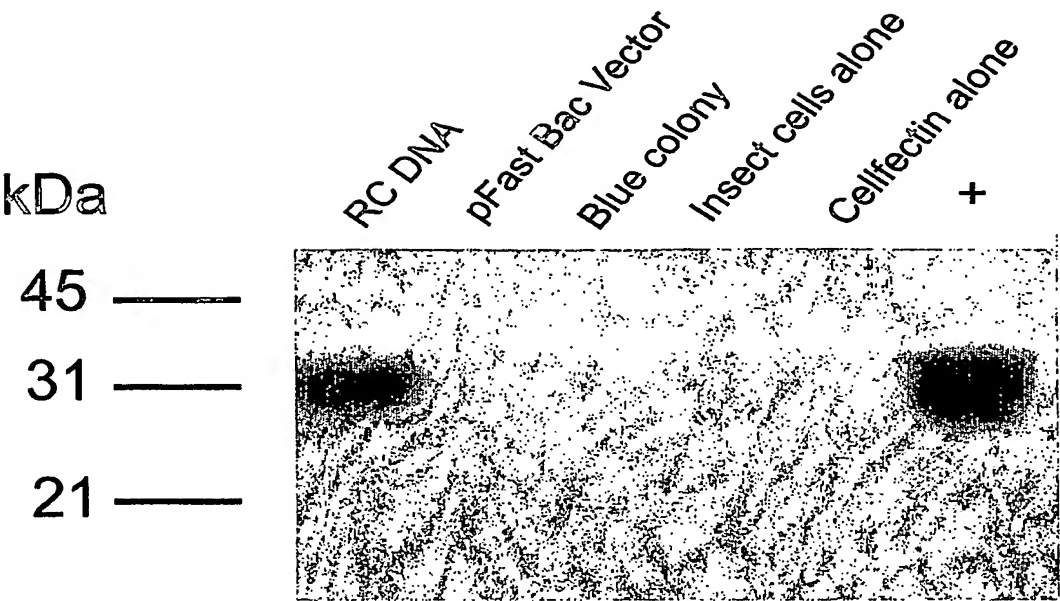


Figure 29A

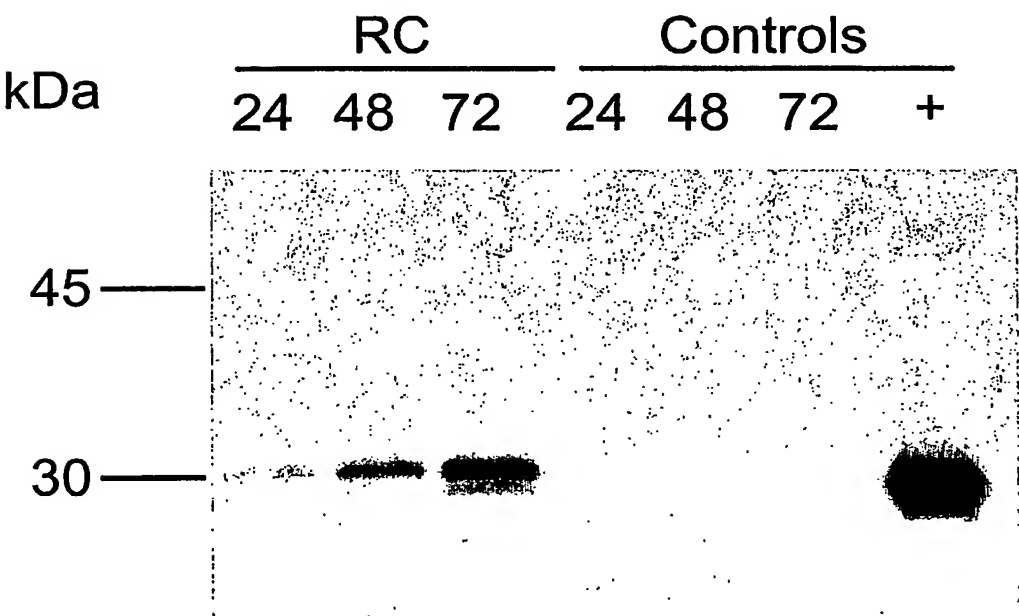


Figure 29B

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